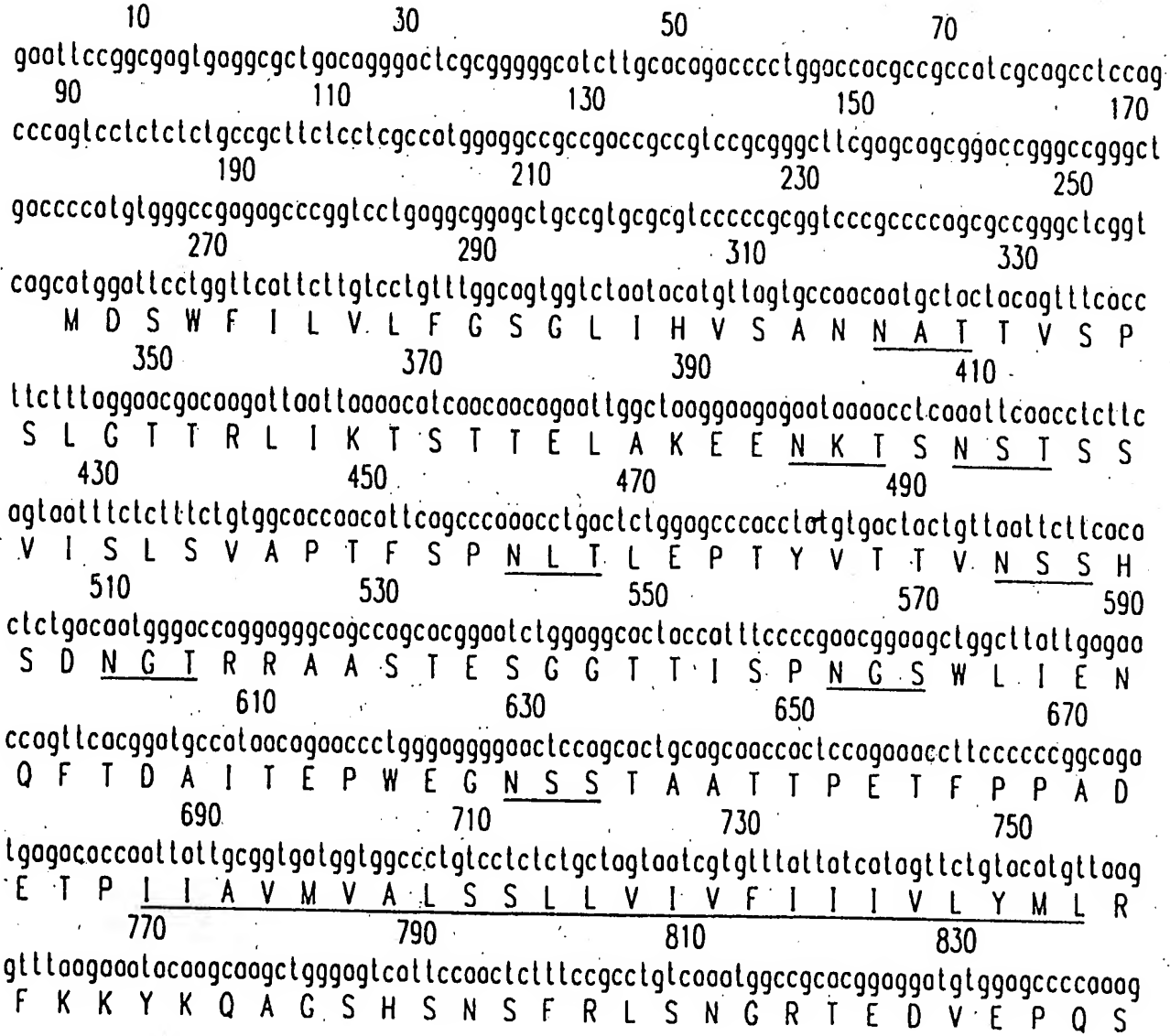


FIG.1A

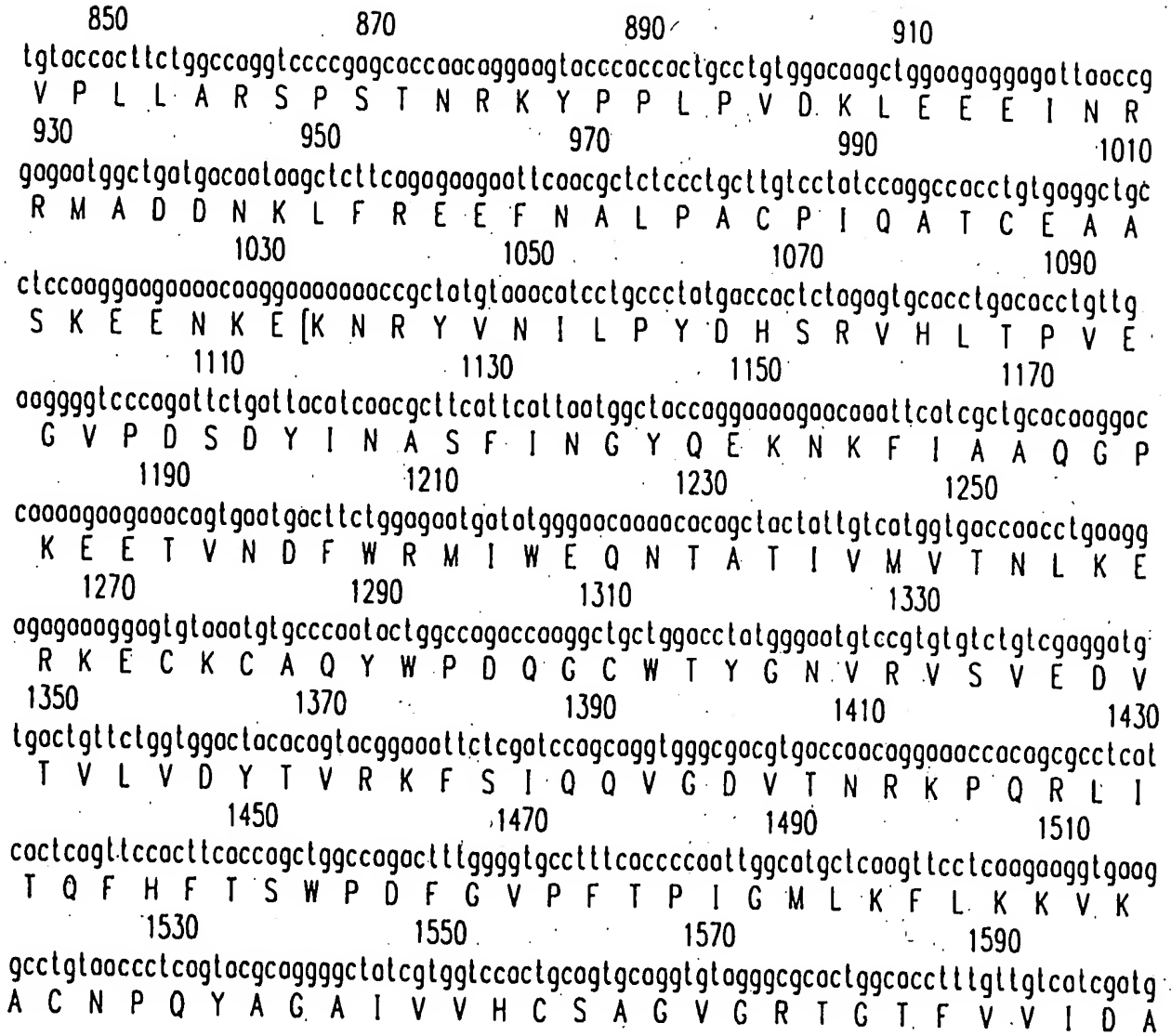


FIG.1B

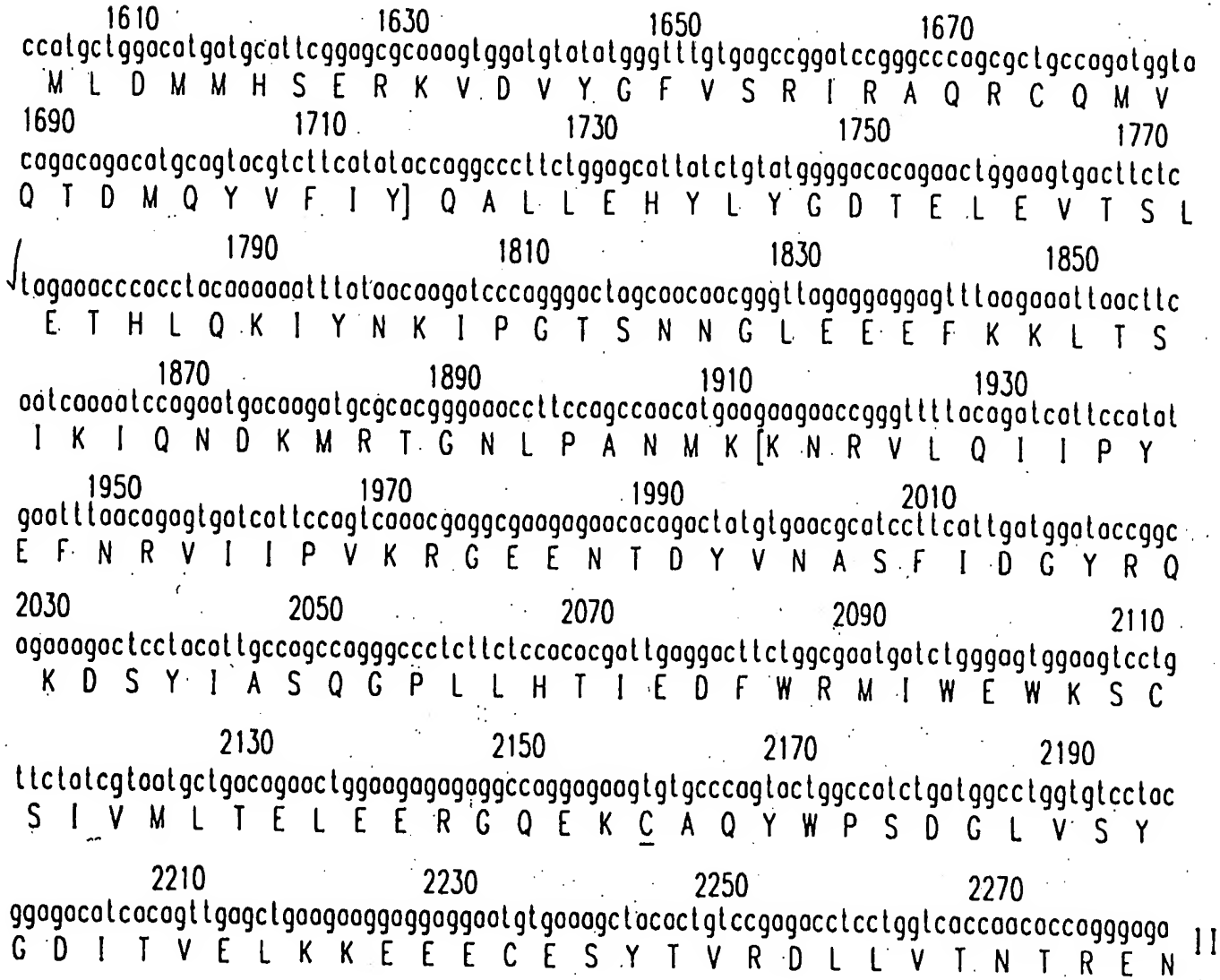


FIG.1C

```
     2290                2310                2330                2350
acaagagtcggcaaatccggcagttccacttccacggctggcctgagggtgggcatccccagcgacggcaagggcatgatcaacat
  K  S  R  Q  I  R  Q  F  H  F  H  G  W  P  E  V  G  I  P  S  D  G  K  G  M  I  N  I

2370                2390                2410                2430                2450
catgcagcagtgcagaagcagcagcagcagtcggggaaccatcccatcactgtgcactgcagtgccggggcaggacggacaggg
  I  A  A  V  Q  K  Q  Q  Q  Q  S  G  N  H  P  I  T  V  H  C  S  A  G  A  G  R  T  G

          2470                2490                2510                2530
accttctgtgccttgagcacagtcctggaacgtgtgaaagcagcaggaattttagatgtcttccaaactgtcaagagcctgcggc
T  F  C  A  L  S  T  V  L  E  R  V  K  A  E  G  I  L  D  V  F  Q  T  V  K  S  L  R  L

          2550                2570                2590                2610
tgcagaggccacacatggtccagacactggaacagtatgaattctgctacaaggtggtacaggaatacattgacgccttttcaga
  Q  R  P  H  M  V  Q  T  L  E  Q  Y  E  F  C  Y] K  V  V  Q  E  Y  I  D  A  F  S  D

     2630                2650                2670                2690
ttatgccaacttcaagtgacaggtgacaaggcccacagacaggagaattgcctttaatattttgtaatattctgttttttgttaat
  Y  A  N  F  K  -.

2710                2730                2750                2770                2790
atacccaaaattgtatatatcttataactgttttagaaatggcacataggcttctattacctgttagatggagattttgtatgta

          2810                2830                2850                2870
aatgtgttagcactgatagtcctttccagtgttttattgggaaattaatagtgtgatatttgggttgatataatgaattc
```

FIG.1D

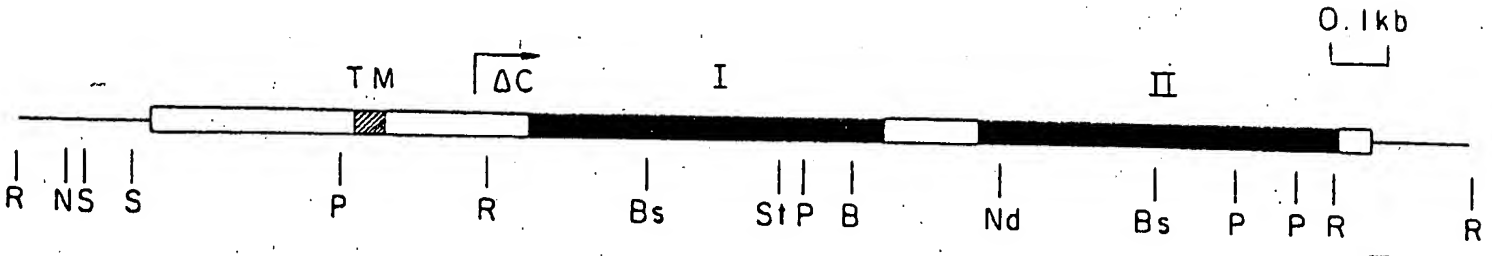


FIG.1E

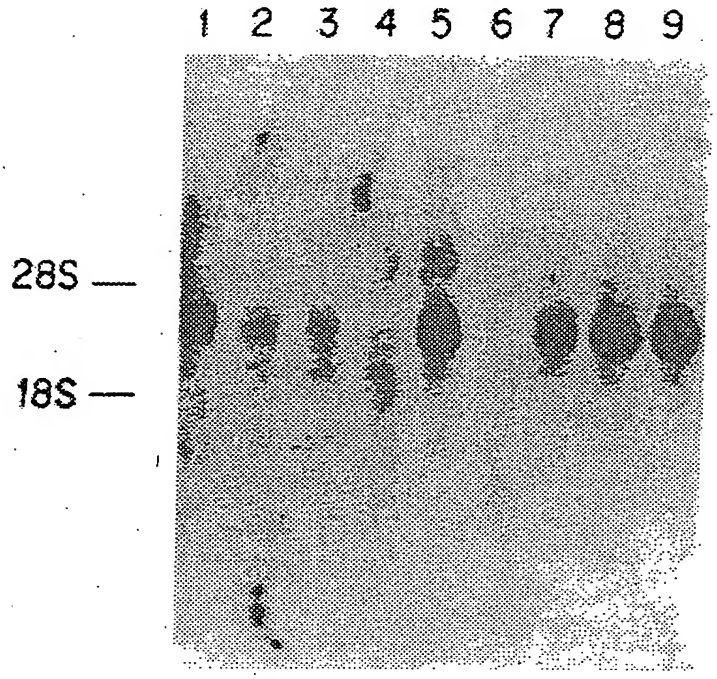


FIG. 2

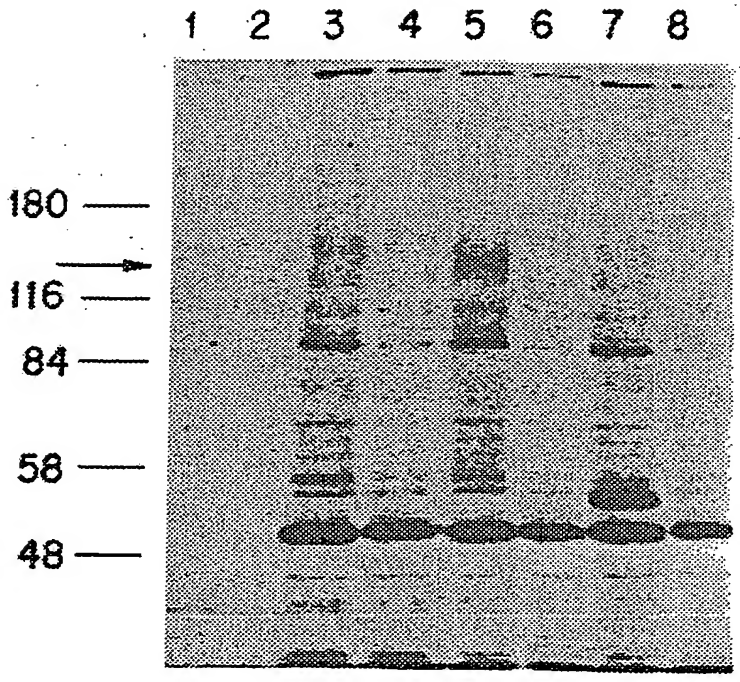


FIG. 3

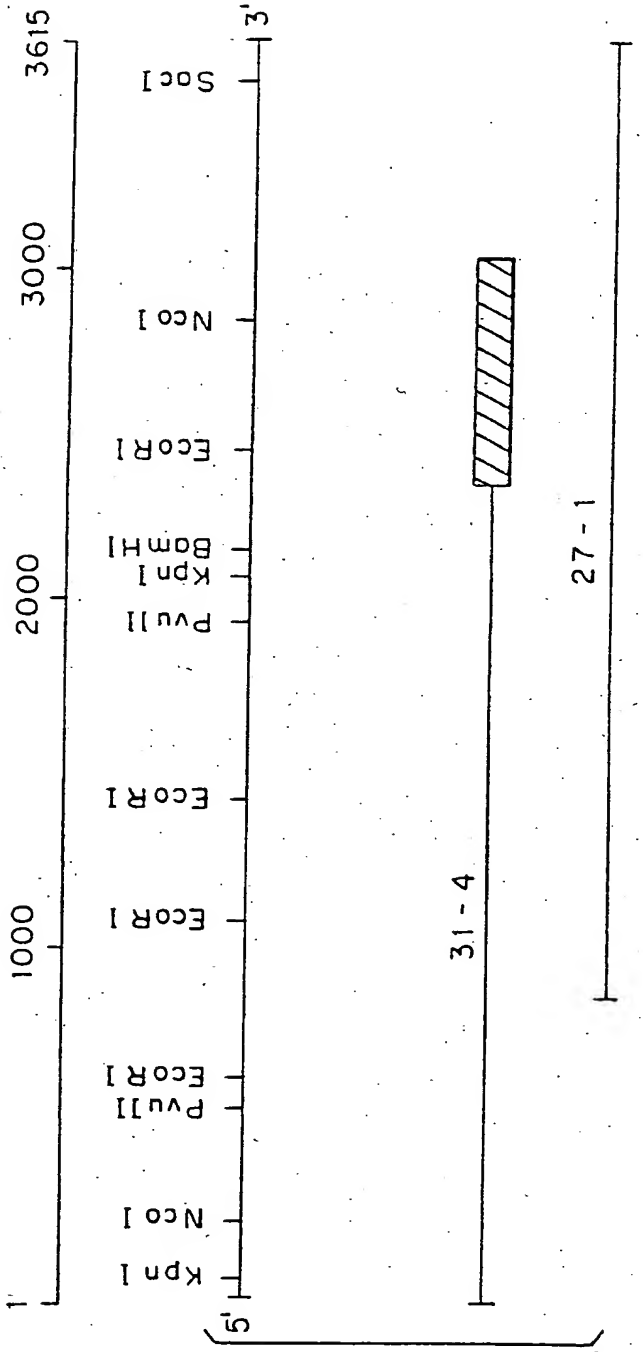


FIG. 4A

FIG. 4B

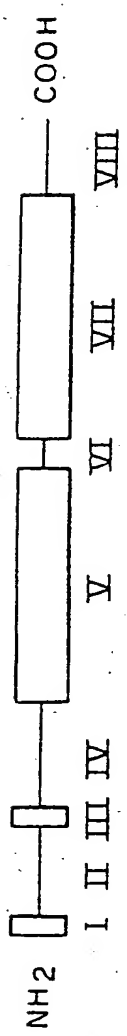


FIG. 4C

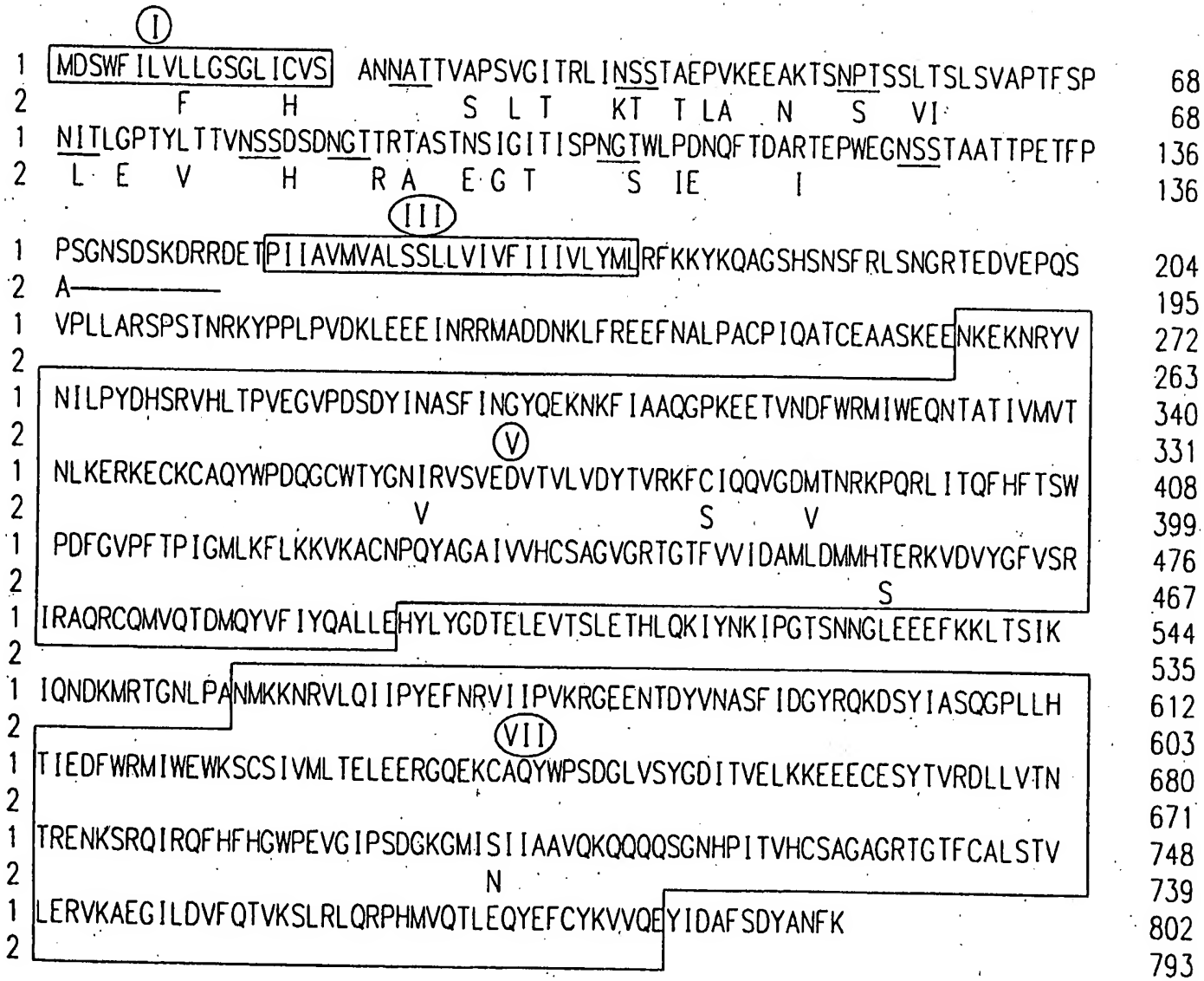


FIG.4D

```
                    10        20        30        40
LCA         NqnKNRYVdILPYDynRVeL  sEinGdagSnYINASyIdGfkEprKyIAA
RPTPase α   NKeKNRYVNILPYDHSRVhLtpvE  GvpdSDYINASfInGYqEknKfIAA
RPTPase β   NKHKNRYINIvAYDHSRVKLaqLaeKDgKItDYINANYVDGYNrpKAYIAA
RPTPase γ   NKHKNRYINIIAYDHSRVKLrpLpgKDsKhsDYINANYVDGYNkaKAYIAt
CON         NkhKNRY-nII-YDhsRVkL--I--k--k-sdYINA-y-dGynepk-yIAa

                    50        60        70        80        90
LCA         QGPrdETVdDFWRMIWEQkatvIVMVTrceEgnrnKCAeYWPsMeegTra
RPTPase α   QGPkeETVnDFWRMIWEQNtatIVMVTNLkErkecKCAQYWPdqGewTYG
RPTPase β   QGPLKSTaEDFWRMIWEhNvevIVMITNLVEKGRRKCDQYWPadGSEEYG
RPTPase γ   QGPLKSTfEDFWRMIWEqNtgiIVMITNLVEKGRRKCDQYWPtenSEEYG
CON         QGPIk-TveDFWRMIWEqnt-vIVM-TnIvEkgrrKC-qYWP--gse-yg

                    100       110       120               130
LCA         fgdVvVkinqhkrcpDYiiqKI     nIvn      kkekatgRevThiq
RPTPase α   NirVsVedVtVLv  DYTVRKFc     IqqvGd   mtnRkpqRIiTQfH
RPTPase β   NfIVTqKSVqVLA  yYTVRnFtIRNTKIKK Gs   qKGRpsgRVVTQYH
RPTPase γ   NiiVTIKStkihAc  YTVRrFsiRNTKvKK GqkgnpKGRqneRVViQYH
CON         ni-Vtvk-v-vIa--dYtvrkf--rntki-k-g-k--kgr--gRvvtqyh
```

FIG.5A

```
                 140       150       160       170       180       190
LCA              FTSWPDhGVPedPhIILKIrrrVnAfsnffsGpIVVHCSAGVGRTGTyigID
                 ||||||  |||  |  ||   | |      | ||||||||||||||   ||
RPTPase α        FTSWPDfGVPftPigmLKFIkKVkAcnpqyaGaIVVHCSAGVGRTGTfvVID
                  | |||  |||     | |  |         |  ||||||||||||  | |
RPTPase β        YTQWPDMGVPEYsLPVLTFVRKaayAkrhavGPVVVHCSAGVGRTGTYIVID
                 ||||||||||| ||||||||    |     | | ||||||||||||||| |
RPTPase γ        YTQWPDMGVPEYaLPVLTFVRrssaArmpetGPVIVHCSAGVGRTGTYIViD

CON              -T-WPDmGVPeypIpvL-fvr-v-aa-----Gp-vVHCSAGVGRTGTyiviD

                      200       210       220       230
LCA              AMLegleaEnKVDVYGyVvkIRrQRCIMVQveaQYiIIhQALvE
                 |||     | ||||||  |   | ||| |||   ||  | ||| |
RPTPase α        AMLdmmhtErKVDVYGFVsrIRaQRCqMVQTdmQYVFIyQALIE
                  ||     |  |   ||   || ||   |||  |||||   | |
RPTPase β        SMLQQIqhEgTVNifGFLKHIRsQRNYLVQTEEQYVFIHDtLvE
                 ||||||   |||  ||||||| |||||||||||| |||| | |
RPTPase γ        SMLQQIkdksTVNvIGFLKHIRtQRNYLVQTEEQYiFIHDaLIE

CON              -MLqqi--e--V-vyGf-khiR-QR-y-VQteeQY-fIh-aL-E
```

FIG.5B

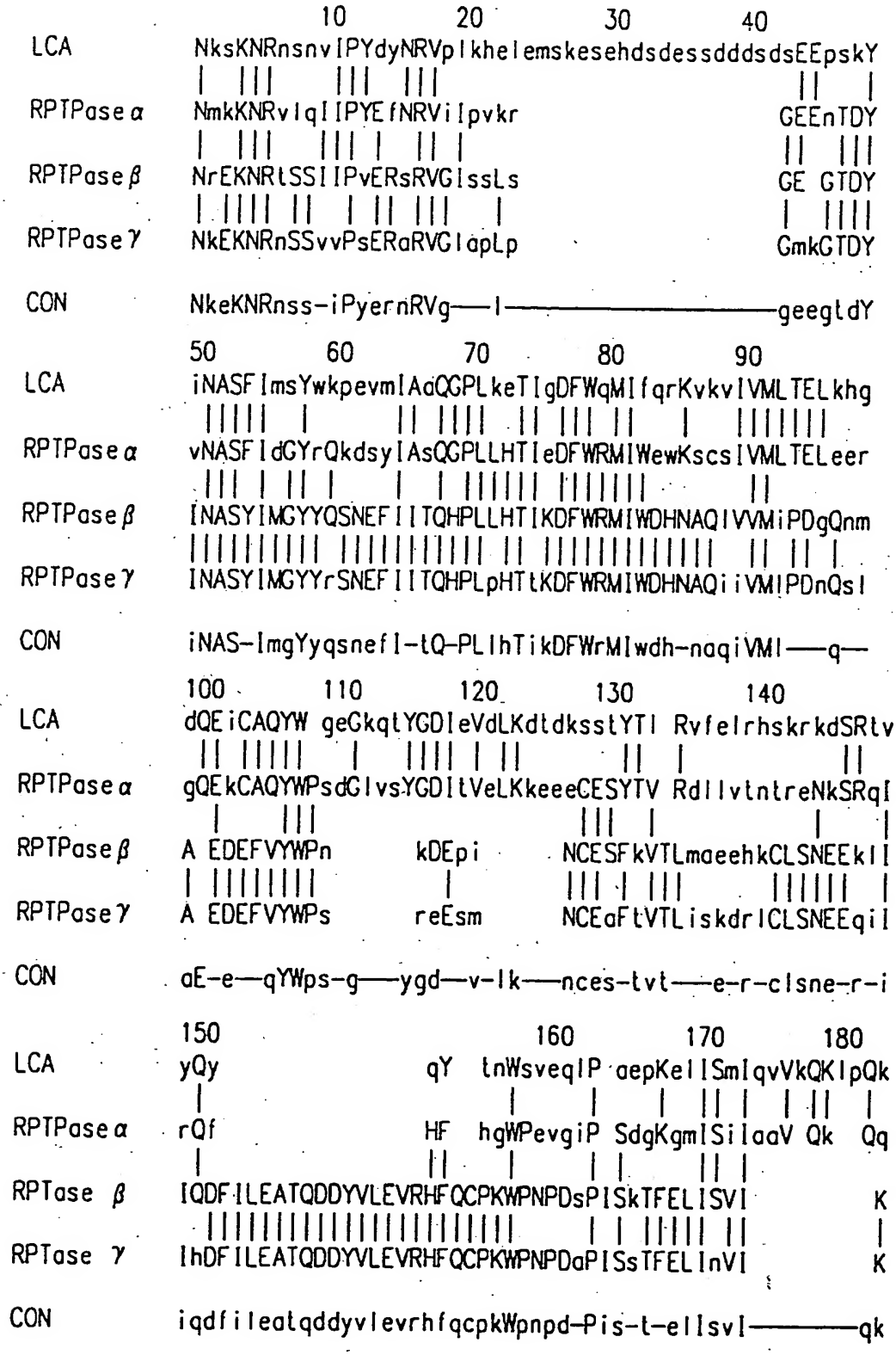

10 20 30 40
LCA NksKNRnsnvIPYdyNRVpIkheIemskesehdsdessdddsdsEEpskY
RPTPase α NmkKNRvIqIIPYEfNRViIpvkr GEEnTDY
RPTPase β NrEKNRtSSIIPvERsRVGIssLs GE GTDY
RPTPase γ NkEKNRnSSvvPsERaRVGIapLp GmkGTDY
CON NkeKNRnss-iPyernRVg——I——————————geegtdY
50 60 70 80 90
LCA iNASFImsYwkpevmIAaQGPLkeTIgDFWqMIfqrKvkvIVMLTELkhg
RPTPase α vNASFIdGYrQkdsyIAsQGPLLHTIeDFWRMIWewKscsIVMLTELeer
RPTPase β INASYIMGYYQSNEFIITQHPLLHTIKDFWRMIWDHNAQIVVMiPDgQnm
RPTPase γ INASYIMGYYrSNEFIITQHPLpHTtKDFWRMIWDHNAQiiVMIPDnQsI
CON iNAS-ImgYyqsnefI-tQ-PLIhTikDFWrMIwdh-naqiVMI——q—
100 110 120 130 140
LCA dQEiCAQYW geGkqtYGDIeVdLKdtdkssIYTI RvfeIrhskrkdSRtv
RPTPase α gQEkCAQYWPsdGIvsYGDItVeLKkeeeCESYTV RdIIvtntreNkSRqI
RPTPase β A EDEFVYWPn kDEpi NCESFkVTLmaeehkCLSNEEkII
RPTPase γ A EDEFVYWPs reEsm NCEaFtVTLiskdrICLSNEEqiI
CON aE-e—qYWps-g——ygd—v-Ik——nces-tvt——e-r-cIsne-r-i
150 160 170 180
LCA yQy qY tnWsveqIP aepKeIISmIqvVkQKIpQk
RPTPase α rQf HF hgWPevgiP SdgKgmISiIaaV Qk Qq
RPTase β IQDFILEATQDDYVLEVRHFQCPKWPNPDsPISkTFELISVI K
RPTase γ IhDFILEATQDDYVLEVRHFQCPKWPNPDaPISsTFELInVI K
CON iqdfileatqddyvIevrhfqcpkWpnpd-Pis-t-eIIsvI——————qk

FIG.5C

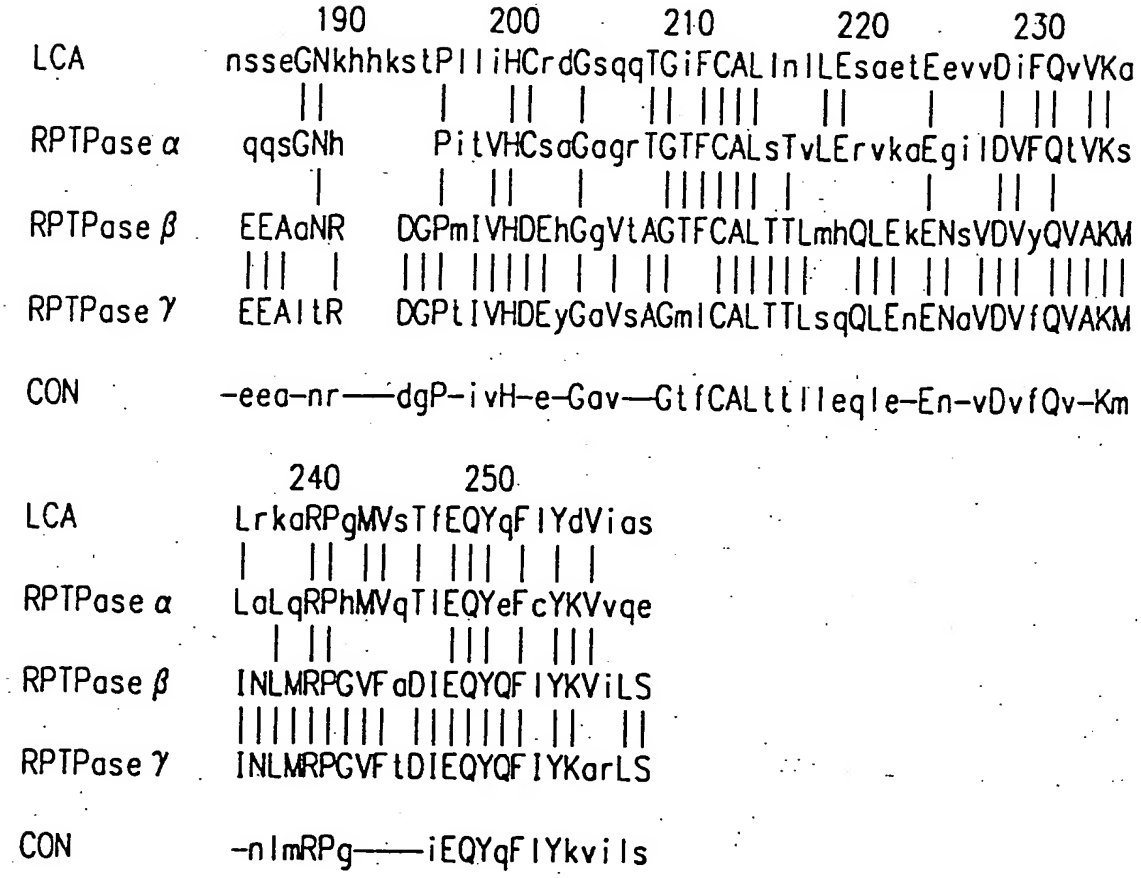

190
200
210
220
230
LCA
nsseGNkhhkstPIIiHCrdGsqqTGiFCALInILEsaetEevvDiFQvVKa
RPTPase α
qqsGNh
PitVHCsaGagrTGTFCALsTvLErvkaEgilDVFQtVKs
RPTPase β
EEAaNR
DGPmIVHDEhGgVtAGTFCALTTLmhQLEkENsVDVyQVAKM
RPTPase γ
EEAItR
DGPtIVHDEyGaVsAGmICALTTLsqQLEnENaVDVfQVAKM
CON
-eea-nr——dgP-ivH-e-Gav—GtfCALttIleqle-En-vDvfQv-Km
240
250
LCA
LrkaRPgMVsTfEQYqFIYdVias
RPTPase α
LaLqRPhMVqTIEQYeFcYKVvqe
RPTPase β
INLMRPGVFaDIEQYQFIYKViLS
RPTPase γ
INLMRPGVFtDIEQYQFIYKarLS
CON
-nlmRPg——iEQYqFIYkvils

FIG.5D

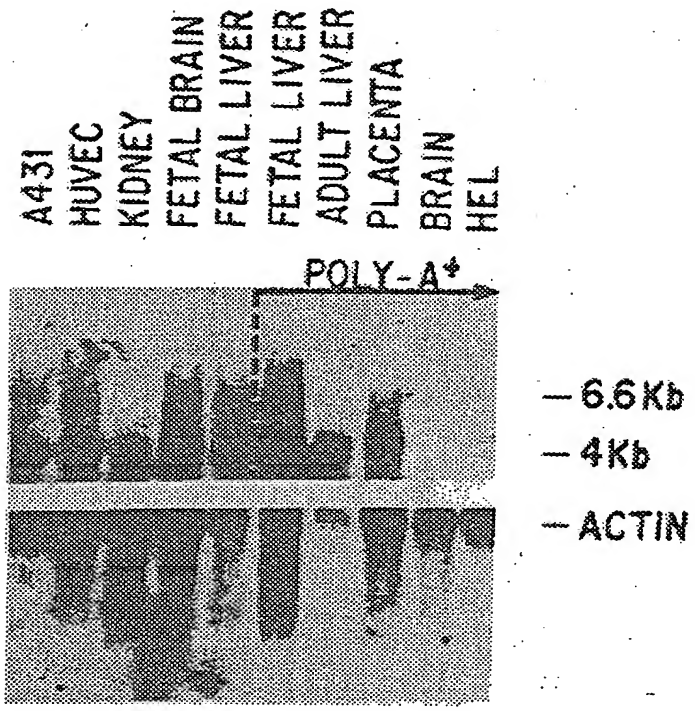
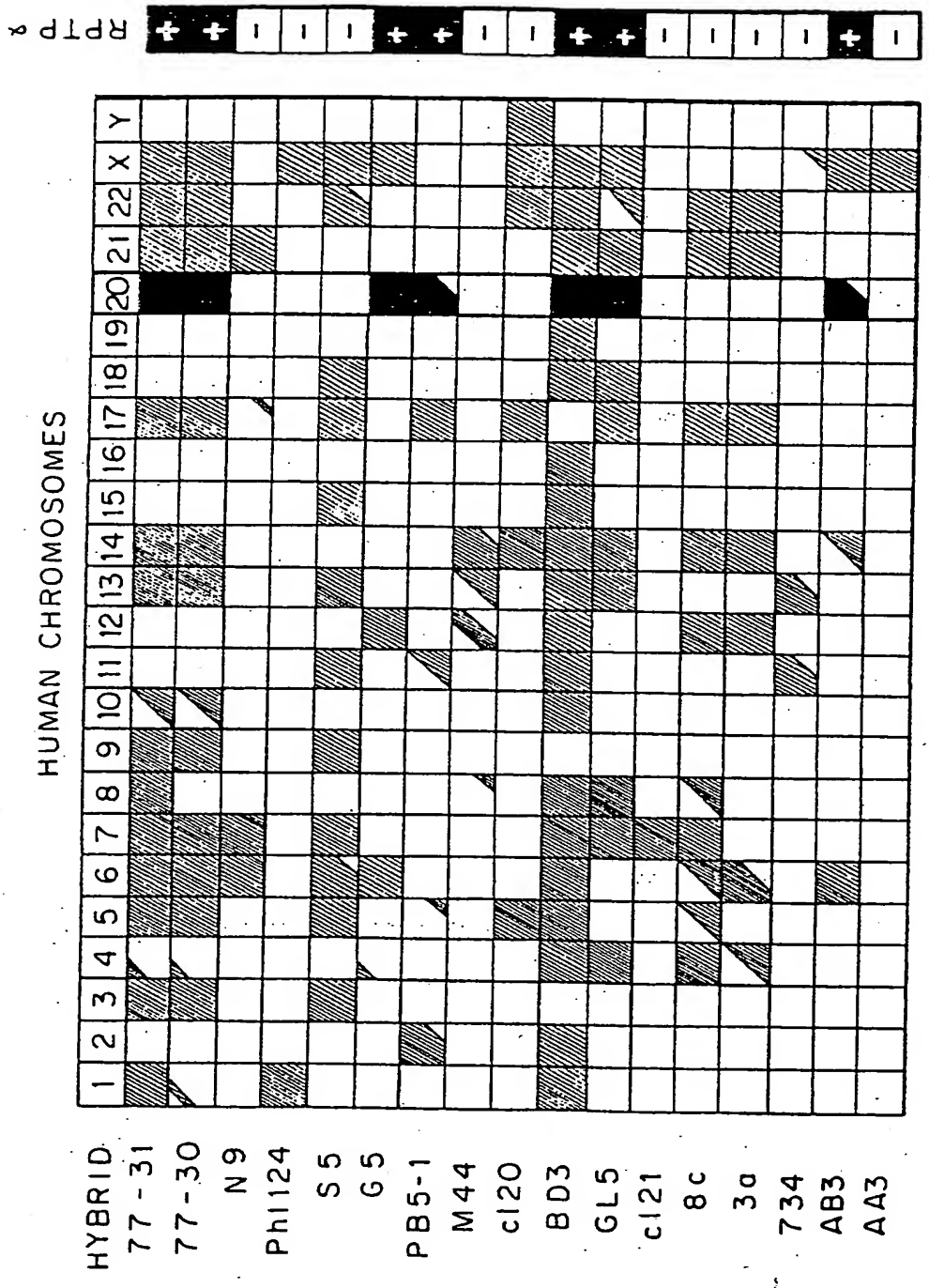

A431
HUVEC
KIDNEY
FETAL BRAIN
FETAL LIVER
FETAL LIVER
ADULT LIVER
PLACENTA
BRAIN
HEL
POLY-A+
6.6Kb
4Kb
ACTIN

FIG. 6

FIG. 7


RPTP α
+ + - - - + + - - + + - - - - + -
HUMAN CHROMOSOMES
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y
HYBRID
77-31
77-30
N9
Ph1124
S5
G5
PB5-1
M44
c120
BD3
GL5
c121
8c
3a
734
AB3
AA3

```
   1 ATGGATTCCTGGTTCATTCTTGTTCTGCTCCGCAGTGGTCTGATATGTGTCAGTGCCAAC  60
   1[M  D  S  W  F  I  L  V  L  L  G  S  G  L  I  C  V  S] A  N   20
     SIGNAL PEPTIDE

  61 AATGCTACCACAGTTGCACCTTCTGTAGGAATTACAAGATTAATTAACTCATCAACGGCA 120
  21 N  A  T  T  V  A  P  S  V  G  I  T  R  L  I  N  S  S  T  A   40

 121 GAACCAGTTAAAGAAGAGGCCAAAACTTCAAATCCAACTTCTTCACTAACTTCTCTTTCT 180
  41 E  P  V  K  E  E  A  K  T  S  N  P  T  S  S  L  T  S  L  S   60

 181 GTGGCACCAACATTCAGCCCAAATATAACTCTGGGACCCACCTATTTAACCACTGTCAAT 240
  61 V  A  P  T  F  S  P  N  I  T  L  G  P  T  Y  L  T  T  V  N   80

 241 TCTTCAGACTCTGACAATGGGACCACAAGAACAGCAAGCACCAATTCTATAGGCATTACA 300
  81 S  S  D  S  D  N  G  T  T  R  T  A  S  T  N  S  I  G  I  T  100

 301 ATTTCACCAAATGGAACGTGGCTTCCAGATAACCAGTTCACGGATGCCAGAACAGAACCC 360
 101 I  S  P  N  G  T  W  L  P  D  N  Q  F  T  D  A  R  T  E  P  120

 361 TGGGAGGGGAATTCCAGCACCGCAGCAACCACTCCAGAAACTTTCCCTCCTTCAGGTAAT 420
 121 W  E  G  N  S  S  T  A  A  T  T  P  E  T  F  P  P  S  G  N  140

 421 TCTGACTCGAAGGACAGAAGAGATGAGACACCAATTATTGCGGTGATGGTGGCCCTGTCC 480
 141 S  D  S  K  D  R  R  D  E  T [P  I  I  A  V  M  V  A  L  S  160
                                  TRANSMEMBRANE SEGMENT

 481 TCTCTGCTAGTGATCGTGTTTATTATCATAGTTTTGTACATGTTAAGGTTTAAGAAATAC 540
 161 S  L  L  V  I  V  F  I  I  I  V  L  Y  M  L] R  F  K  K  Y  180

 541 AAGCAAGCTGGGAGCCATTCCAATTCTTTCCGCTTATCCAACGGCCGCACTGAGGATGTG 600
 181 K  Q  A  G  S  H  S  N  S  F  R  L  S  N  G  R  T  E  D  V  200

 601 GAGCCCCAGAGTGTGCCACTTCTGGCCAGATCCCCAAGCACCAACAGGAAATACCCACCC 660
 201 E  P  Q  S  V  P  L  L  A  R  S  P  S  T  N  R  K  Y  P  P  220

 661 CTGCCCGTGGACAAGCTGGAAGAGGAAATTAACCGGAGAATGGCAGACGACAATAAGCTC 720
 221 L  P  V  D  K  L  E  E  E  I  N  R  R  M  A  D  D  N  K  L  240

 721 TTCAGGGAGGAATTCAACGCTCTCCCTGCATGTCCTATCCAGGCCACCTGTGAGGCTGCT 780
 241 F  R  E  E  F  N  A  L  P  A  C  P  I  Q  A  T  C  E  A  A  260

 781 TCCAAGGAGGAAAACAAGGAAAAAAATCGATATGTAAACATCTTGCCTTATGACCACTCT 840
 261 S  K  E  E [N  K  E  K  N  R  Y  V  N  I  L  P  Y  D  H  S  280
     PTPase DOMAIN I
```

FIG.8A

```
841 AGAGTCCACCTGACACCGGTTGAAGGGGTTCCAGATTCTGATTACATCAATGCTTCATTC  900
281 R  V  H  L  T  P  V  E  G  V  P  D  S  D  Y  I  N  A  S  F   300

901 ATCAACGGTTACCAAGAAAAGAACAAATTCATTGCTGCACAAGGACCAAAAGAAGAAACG  960
301 I  N  G  Y  Q  E  K  N  K  F  I  A  A  Q  G  P  K  E  E  T   320

961 GTGAATGATTTCTGGCGGATGATCTGGGAACAAAACACAGCCACCATCGTCATGGTTACC 1020
321 V  N  D  F  W  R  M  I  W  E  Q  N  T  A  T  I  V  M  V  T   340

1021 AACCTGAAGGAGAGAAAGGAGTGCAAGTGCGCCCAGTACTGGCCAGACCAAGGCTGCTGG 1080
341 N  L  K  E  R  K  E  C  K  C  A  Q  Y  W  P  D  Q  G  C  W   360

1081 ACCTATGGGAATATTCGGGTGTCTGTAGAGGATGTGACTGTCCTGGTGGACTACACAGTA 1140
361 T  Y  G  N  I  R  V  S  V  E  D  V  T  V  L  V  D  Y  T  V   380

1141 CGGAAGTTCTGCATCCAGCAGGTGGGCGACATGACCAACAGAAAGCCACAGCGCCTCATC 1200
381 R  K  F  C  I  Q  Q  V  G  D  M  T  N  R  K  P  Q  R  L  I   400

1201 ACTCAGTTCCACTTTACCAGCTGGCCAGACTTTGGGGTGCCTTTTACCCCGATCGGCATG 1260
401 T  Q  F  H  F  T  S  W  P  D  F  G  V  P  F  T  P  I  G  M   420

1261 CTCAAGTTCCTCAAGAAGGTGAAGGCCTGTAACCCTCAGTATGCAGGGGCCATCGTGGTC 1320
421 L  K  F  L  K  K  V  K  A  C  N  P  Q  Y  A  G  A  I  V  V   440

1321 CACTGCAGTGCAGGTGTAGGGCGTACAGGTACCTTTGTCGTCATTGATGCCATGCTGGAC 1380
441 H  C  S  A  G  V  G  R  T  G  T  F  V  V  I  D  A  M  L  D   460

1381 ATGATGCATACAGAACGGAAGGTGGACGTGTATGGCTTTGTGAGCCGGATCCGGGCACAG 1440
461 M  M  H  T  E  R  K  V  D  V  Y  G  F  V  S  R  I  R  A  Q   480

1441 CGCTGCCAGATGGTGCAAACCGATATGCAGTATGTCTTCATATACCAAGCCCTTCTGGAG 1500
481 R  C  Q  M  V  Q  T  D  M  Q  Y  V  F  I  Y  Q  A  L  L  E]  500

1501 CATTATCTCTATGGAGATACAGAACTGGAAGTGACCTCTCTAGAAACCCACCTGCAGAAA 1560
501 H  Y  L  Y  G  D  T  E  L  E  V  T  S  L  E  T  H  L  Q  K   520

1561 ATTTACAACAAAATCCCAGGGACCAGCAACAATGGATTAGAGGAGGAGTTTAAGAAGTTA 1620
521 I  Y  N  K  I  P  G  T  S  N  N  G  L  E  E  E  F  K  K  L   540
```

FIG.8B

```
1621 ACATCAATCAAAATCCAGAATGACAAGATGCGGACTGGAAACCTTCCAGCCAACATGAAG 1680
 541 T  S  I  K  I  Q  N  D  K  M  R  T  G  N  L  P  A [N  M  K   560
                                                        PTPase Domain II
1681 AAGAACCGTGTTTTACAGATCATTCCATATGAATTCAACAGAGTGATCATTCCAGTTAAG 1740
 561 K  N  R  V  L  Q  I  I  P  Y  E  F  N  R  V  I  I  P  V  K   580

1741 CGGGGCGAAGAGAATACAGACTATGTGAACGCATCCTTTATTGATGGCTACCGGCAGAAG 1800
 581 R  G  E  E  N  T  D  Y  V  N  A  S  F  I  D  G  Y  R  Q  K   600

1801 GACTCCTATATCGCCAGCCAGGGCCCTCTTCTCCACACAATTGAGGACTTCTGGCGAATG 1860
 601 D  S  Y  I  A  S  Q  G  P  L  L  H  T  I  E  D  F  W  R  M   620

1861 ATCTGGGAGTGGAAATCCTGCTCTATCGTGATGCTAACAGAACTGGAGGAGAGAGGCCAG 1920
 621 I  W  E  W  K  S  C  S  I  V  M  L  T  E  L  E  E  R  G  Q   640

1921 GAGAAGTGTGCCCAGTACTGGCCATCTGATGGACTGGTGTCCTATGGAGATATTACAGTG 1980
 641 E  K  C  A  Q  Y  W  P  S  D  G  L  V  S  Y  G  D  I  T  V   660

1981 GAACTGAAGAAGGAGGAGGAATGTGAGAGCTACACCGTCCGAGACCTCCTGGTCACCAAC 2040
 661 E  L  K  K  E  E  E  C  E  S  Y  T  V  R  D  L  L  V  T  N   680

2041 ACCAGGGAGAATAAGAGCCGGCAGATCCGGCAGTTCCACTTCCATGGCTGGCCTGAAGTG 2100
 681 T  R  E  N  K  S  R  Q  I  R  Q  F  H  F  H  G  W  P  E  V   700

2101 GGCATCCCCAGTGACGGAAAGGGCATGATCAGCATCATCGCCGCCGTGCAGAAGCAGCAG 2160
 701 G  I  P  S  D  G  K  G  M  I  S  I  I  A  A  V  Q  K  Q  Q   720

2161 CAGCAGTCAGGGAACCACCCCATCACCGTGCACTGCAGCGCCGGGGCAGGAAGGACGGGG 2220
 721 Q  Q  S  G  N  H  P  I  T  V  H  C  S  A  G  A  G  R  T  G   740

2221 ACCTTCTGTGCCCTGAGCACCGTCCTGGAGCGTGTGAAAGCAGAGGGGATTTTGGATGTC 2280
 741 T  F  C  A  L  S  T  V  L  E  R  V  K  A  E  G  I  L  D  V   760

2281 TTCCAGACTGTCAAGAGCCTGCGGCTACAGAGGCCACACATGGTCCAGACACTGGAACAG 2340
 761 F  Q  T  V  K  S  L  R  L  Q  R  P  H  M  V  Q  T  L  E  Q   780

2341 TATGAGTTCTGCTACAAGGTGGTGCAGGAGTATATTGATGCATTCTCAGATTATGCCAAC 2400
 781 Y  E  F  C  Y  K  V  V  Q  E] Y  I  D  A  F  S  D  Y  A  N   800

2401 TTCAAGTAA 2409
 801 F  K  *   803
```

FIG.8C